

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5 (i) APPLICANTS: Chatterjee, Deb K.  
Solus, Joseph  
Yang, Shuwei

(ii) TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic  
Nucleic Acid Fragments and Uses Thereof

(iii) NUMBER OF SEQUENCES: 93

## 10 (iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington  
(D) STATE: DC  
15 (E) COUNTRY: USA  
(F) ZIP: 20005-3934

## (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)  
(B) FILING DATE: 06-FEB-1998  
25 (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: (To be assigned)  
(B) FILING DATE: 06-JAN-1998  
(C) CLASSIFICATION:

## 30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/037,393  
(B) FILING DATE: 07-FEB-1997  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0942.4250002

## (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 202-371-2600  
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## (2) INFORMATION FOR SEQ ID NO:1:

SEQUENCE LISTING

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2682 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 5 (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGAGAC	TATTTCTCTT	TGATGGCACA	GCCCTGGCCT	ACAGGGCATA	TTACGCCCTC	60
GACAGATCCC	TTTCCACATC	CACAGGAATT	CCAACGAACG	CCGTCTATGG	CGTTGCCAGG	120
10 ATGCTCGTTA	AATTCAATTAA	GGAACACATT	ATACCCGAAA	AGGACTACGC	GGCTGTGGCC	180
TTCGACAAGA	AGGCAGCGAC	GTTCAGACAC	AAACTGCTCG	TAAGCGACAA	GGCGCAAAGG	240
CCAAAGACTC	CGGCTCTTCT	AGTTCAAGCAG	CTACCTTACA	TCAAGCGGCT	GATAGAAGCT	300
CTTGGTTTCA	AAGTGCTGGA	GCTGGAGGGG	TACGAAGCAG	ACGATATCAT	CGCCACGCTT	360
GCAGTCAGGG	CTGCACGTTT	TTTGATGAGA	TTTCATTAA	TAACCGGTGA	CAAGGATATG	420
15 CTTCAACTTG	TAAACGAGAA	GATAAAGGTC	TGGAGAATCG	TCAAGGGGAT	ATCGGATCTT	480
GAGCTTTACG	ATTCGAAAAAA	GGTGAAAGAA	AGATACTGGTG	TGGAACCACA	TCAGATACCG	540
GATCTTCTAG	CACTGACGGG	AGACGACATA	GACAACATTG	CCGGTGTAAAC	GGGAATAGGT	600
GAAAAGACCG	CTGTACAGCT	TCTCGGCAAG	TATAGAAATC	TTGAATACAT	TCTGGAGCAT	660
GCCC GTGAAC	TCCCCCAGAG	AGTGAGAAAG	GCTCTCTTGA	GAGACAGGGG	AGTTGCCATC	720
20 CTCAGTAAAA	AACTTGCAAC	TCTGGTGACG	AACGCACCTG	TTGAAGTGGG	CTGGGAAGAG	780
ATGAAATACA	GAGGATACGA	CAAGAGAAAA	CTACTTCCGA	TATTGAAAGA	ACTGGAGTTT	840
GCTTCCATCA	TGAAGGAACT	TCAACTGTAC	GAAGAAGCAG	AACCCACCGG	ATACGAAATC	900
GTGAAGGATC	ATAAGACCTT	CGAAGATCTC	ATCGAAAAGC	TGAAGGAGGT	TCCATCTTT	960
GCCCTGGACC	TTGAAACGTC	CTCCCTTGAC	CCGTTCAACT	GTGAGATAGT	CGGCATCTCC	1020
25 GTGTCGTTCA	AACCGAAAAC	AGCTTATTAC	ATTCCACTTC	ATCACAGAAA	CGCCCAGAAT	1080
CTTGATGAAA	CACTGGTGCT	GTCGAAGTTG	AAAGAGATCC	TCGAAGACCC	GTCTTCGAAG	1140
ATTGTGGTC	AGAACCTGAA	GTACGACTAC	AAGGTTCTTA	TGGTAAAGGG	TATATGCCA	1200
GTTTATCCGC	ATTTTGACAC	GATGATAGCT	GCATATTTGC	TGGAGCCAAA	CGAGAAAAAA	1260
TTCAATCTCG	AAGATCTGTC	TTTGAAATTT	CTCGGATACA	AAATGACGTC	TTATCAGGAA	1320

SEQUENCE ID: 20

CTGATGTCGT	TTTCCTCACC	ACTTTTGTT	TTCAGCTTG	CGGATGTTCC	GGTAGACAAG	1380	
GCTGCGAACT	ACTCCTGCGA	GGATGCAGAC	ATCACTTATA	GGCTCTACAA	GATACTCAGC	1440	
ATGAAGCTCC	ATGAAGCGGA	ACTTGAGAAC	GTCTTCTACA	GGATAGAGAT	GCCGTTGGTG	1500	
AACGTTCTTG	CACGCATGGA	ATTGAACGGG	GTGTATGTGG	ACACAGAATT	CCTGAAAAAG	1560	
5	CTCTCGGAGG	AGTACGGCAA	AAAGCTCGAG	GAACGGCCG	AAAAAATCTA	CCAGATAGCA	1620
	GGTGAGCCCT	TCAACATCAA	TTCTCCAAAA	CAGGTTTCAA	AGATCCTTTT	TGAGAAGCTG	1680
	GGAATAAAAC	CCCGTGGAAA	AACGACAAAAA	ACAGGAGAGT	ACTCTACCA	GATAGAGGTG	1740
	TTGGAAGAGA	TAGCGAATGA	GCACGAGATA	GTACCCCTCA	TTCTCGAGTA	CAGAAAGATC	1800
	CAGAAACTGA	AATCGACCTA	CATAGACACC	CTTCCGAAAC	TTGTGAACCC	GAAAACCGGA	1860
10	AGAATTCATG	CATCTTCCA	CCAGACGGGT	ACCGCCACTG	GCAGGTTGAG	TAGCAGTGAT	1920
	CCAAATCTTC	AGAATCTTCC	GACAAAGAGC	GAAGAGGGAA	AAGAAATTAG	AAAAGCGATT	1980
	GTGCCCCAGG	ATCCAGACTG	GTGGATCGTC	AGTGCAGGATT	ATTCCCAAAT	AGAACTCAGA	2040
	ATCCTCGCTC	ATCTCAGTGG	TGATGAGAAC	CTTGTGAAGG	CCTTCGAGGA	GGGCATCGAT	2100
	GTGCACACCT	TGACTGCCTC	CAGGATCTAC	AACGTAAAGC	CAGAAGAAGT	GAACGAAGAA	2160
15	ATGCGACGGG	TTGGAAAGAT	GGTGAACCTC	TCTATAATAT	ACGGTGTAC	ACCGTACGGT	2220
	CTTTCTGTGA	GACTTGAAT	ACCGGTTAAA	GAAGCAGAAA	AGATGATTAT	CAGCTATTTC	2280
	ACACTGTATC	CAAAGGTGCG	AAGCTACATC	CAGCAGGTTG	TTGCAGAGGC	AAAAGAGAAG	2340
	GGCTACGTCA	GGACTCTCTT	TGGAAGAAAA	AGAGATATTC	CCCAGCTCAT	GGCAAGGGAC	2400
	AAGAACACCC	AGTCCGAAGG	CGAAAGAATC	GCAATAAACCA	CCCCCATTCA	GGGAACGGCG	2460
20	GCAGATATAA	AAAAATTGGC	TATGATAGAT	ATAGACGAGG	AGCTGAGAAA	AAGAAACATG	2520
	AAATCCAGAA	TGATCATTCA	GGTCATGAC	GAACGGTCT	TCGAGGTTCC	CGATGAGGAA	2580
	AAAGAAGAAC	TAGTTGATCT	GGTGAAGAAC	AAAATGACAA	ATGTGGTGAA	ACTCTCTGTG	2640
	CCTCTTGAGG	TTGACATAAG	CATCGGAAAAA	AGCTGGTCTT	GA		2682

## (2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala			
1	5	10	15

5	Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr		
	20	25	30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu			
35	40	45	

10	His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys		
	50	55	60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg			
65	70	75	80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg			
	85	90	95

15	Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu		
	100	105	110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu			
115	120	125	

20	Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val		
	130	135	140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu			
145	150	155	160

Glu Leu Tyr Asp Ser Lys Val Lys Glu Arg Tyr Gly Val Glu Pro			
165	170	175	

25	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn		
	180	185	190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu			
195	200	205	

30	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu		
	210	215	220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile			
225	230	235	240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val			
245	250	255	

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285

5 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320

10 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365

15 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400

20 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445

25 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480

30 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525

35 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu

	545	550	555	560
	Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr			
	565	570	575	
5	Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Ile Val Pro			
	580	585	590	
	Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile			
	595	600	605	
	Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala			
	610	615	620	
10	Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp			
	625	630	635	640
	Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile			
	645	650	655	
15	Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala			
	660	665	670	
	Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp			
	675	680	685	
	Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu			
	690	695	700	
20	Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu			
	705	710	715	720
	Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val			
	725	730	735	
25	Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala			
	740	745	750	
	Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser			
	755	760	765	
	Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg			
	770	775	780	
30	Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp			
	785	790	795	800
	Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile			
	805	810	815	
35	Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp			
	820	825	830	
	Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val			
	835	840	845	

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880

5 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
 885 890

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 677 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Leu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu  
 1 5 10 15

Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu  
 20 25 30

Val Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg  
 35 40 45

Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe  
 50 55 60

Ala Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr  
 65 70 75 80

25 Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu  
 85 90 95

Lys Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser  
 100 105 110

Leu Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys  
 115 120 125

Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn  
 130 135 140

Leu Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp  
 145 150 155 160

Pro Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val  
 165 170 175

Leu Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met  
 180 185 190

5 Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu  
 195 200 205

Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu  
 210 215 220

10 Leu Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val  
 225 230 235 240

Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr  
 245 250 255

Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu  
 260 265 270

15 Glu Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala  
 275 280 285

Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys  
 290 295 300

20 Leu Ser Glu Glu Tyr Gly Lys Leu Glu Glu Leu Ala Glu Lys Ile  
 305 310 315 320

Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val  
 325 330 335

Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr  
 340 345 350

25 Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile  
 355 360 365

Ala Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile  
 370 375 380

30 Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn  
 385 390 395 400

Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala  
 405 410 415

Thr Gly Arg Leu Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr  
 420 425 430

35 Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp  
 435 440 445

Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg

	450	455	460
	Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu		
	465	470	475
	Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val		
5	485	490	495
	Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val		
	500	505	510
	Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg		
	515	520	525
10	Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe		
	530	535	540
	Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu		
	545	550	555
	560		
15	Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp		
	565	570	575
	Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu		
	580	585	590
	Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile		
	595	600	605
20	Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met		
	610	615	620
	Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val		
	625	630	635
	640		
25	Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met		
	645	650	655
	Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile		
	660	665	670
	Gly Lys Ser Trp Ser		
	675		

30 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 610 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Lys	Glu	Leu	Gln	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	
1																	15
	Ile	Val	Lys	Asp	His	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	
5																	30
	Glu	Val	Pro	Ser	Phe	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	
	35																45
	Phe	Asn	Cys	Glu	Ile	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	
10	50																60
	Ala	Tyr	Tyr	Ile	Pro	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	
	65																80
	Thr	Leu	Val	Leu	Ser	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	
	85																95
15	Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	
	100																110
	Lys	Gly	Ile	Ser	Pro	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	
	115																125
	Tyr	Leu	Leu	Glu	Pro	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	
	130																140
20	Leu	Lys	Phe	Leu	Gly	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	
	145																160
	Phe	Ser	Ser	Pro	Leu	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	
	165																175
25	Lys	Ala	Ala	Asn	Tyr	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	
	180																190
	Tyr	Lys	Ile	Leu	Ser	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	
	195																205
	Phe	Tyr	Arg	Ile	Glu	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	
	210																220
30	Leu	Asn	Gly	Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	
	225																240
	Glu	Tyr	Gly	Lys	Lys	Leu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile		
	245																255
35	Ala	Gly	Glu	Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	
	260																270
	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	

	275	280	285
	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu		
	290	295	300
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu		
5	305	310	315
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr		
	325	330	335
	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg		
	340	345	350
10	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu		
	355	360	365
	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp		
	370	375	380
15	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala		
	385	390	395
	His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile		
	405	410	415
	Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu		
	420	425	430
20	Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser		
	435	440	445
	Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile		
	450	455	460
25	Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr		
	465	470	475
	Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu		
	485	490	495
30	Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln		
	500	505	510
	Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala		
	515	520	525
	Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala		
	530	535	540
35	Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg		
	545	550	555
	Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu		

565

570

575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
 580 585 590

5 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
 595 600 605

Trp Ser  
 610

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 708 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu  
 1 5 10 15

Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile  
 20 25 30

20 Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu  
 35 40 45

Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val  
 50 55 60

25 Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly  
 65 70 75 80

Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala  
 85 90 95

Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly  
 100 105 110

30 Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys  
 115 120 125

Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu  
 130 135 140

Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro

145	150	155	160	
Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu				
165		170	175	
Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro				
5	180	185	190	
Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu				
195		200	205	
Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile				
210		215	220	
10	Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp	225	230	
235				240
Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu				
245		250	255	
15	Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro	260	265	
270				
Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr				
275		280	285	
Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu				
290		295	300	
20	Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg	305	310	
315				320
Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu				
325		330	335	
25	Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr	340	345	
350				
Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser				
355		360	365	
Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr				
370		375	380	
30	Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala	385	390	
395				400
Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln				
405		410	415	
35	Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro	420	425	
430				
Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr				

	435	440	445
	Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys		
	450	455	460
5	Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro		
	465	470	475
	Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile		
	485	490	495
	Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu		
	500	505	510
10	Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys		
	515	520	525
	Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn		
	530	535	540
15	Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu		
	545	550	555
	Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr		
	565	570	575
	Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala		
	580	585	590
20	Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile		
	595	600	605
	Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg		
	610	615	620
25	Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys		
	625	630	635
	Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys		
	645	650	655
	Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro		
	660	665	670
30	Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr		
	675	680	685
	Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly		
	690	695	700
35	Lys Ser Trp Ser		
	705		

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 893 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

5

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala	
	1 5 10 15	
10	Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr	
	20 25 30	
	Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu	
	35 40 45	
15	His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys	
	50 55 60	
	Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg	
	65 70 75 80	
	Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg	
	85 90 95	
20	Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu	
	100 105 110	
	Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu	
	115 120 125	
25	Met Arg Phe Ser Leu Ile Thr Gly Ala Lys Asp Met Leu Gln Leu Val	
	130 135 140	
	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu	
	145 150 155 160	
	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro	
	165 170 175	
30	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn	
	180 185 190	
	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu	
	195 200 205	
35	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu	
	210 215 220	

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255

5 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285

Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 10 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320

Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335

15 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 20 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400

Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415

25 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 30 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480

Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495

35 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys		
515	520	525
Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe		
530	535	540
5 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu		
545	550	555
Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr		
565	570	575
10 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro		
580	585	590
Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile		
595	600	605
Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala		
610	615	620
15 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp		
625	630	635
Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile		
645	650	655
20 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala		
660	665	670
Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp		
675	680	685
Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu		
690	695	700
25 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu		
705	710	715
Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val		
725	730	735
30 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala		
740	745	750
Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser		
755	760	765
Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg		
770	775	780
35 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp		
785	790	795
800		

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815  
 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
 820 825 830  
 5 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
 835 840 845  
 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Leu  
 850 855 860  
 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
 10 865 870 875 880  
 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
 885 890

## (2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Leu Phe Leu Phe Ala Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15  
 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30  
 25 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45  
 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60  
 30 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80  
 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95  
 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110  
 35 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu

	115	120	125
	Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp	Met Leu Gln Leu Val	
	130	135	140
	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu		
5	145	150	155
	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro		
	165	170	175
	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn		
	180	185	190
10	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu		
	195	200	205
	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu		
	210	215	220
15	Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile		
	225	230	235
	Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val		
	245	250	255
	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu		
	260	265	270
20	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln		
	275	280	285
	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His		
	290	295	300
25	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe		
	305	310	315
	Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile		
	325	330	335
	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro		
	340	345	350
30	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser		
	355	360	365
	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln		
	370	375	380
35	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro		
	385	390	395
	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro		
	405	410	415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 435 440 445

5 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480

10 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525

15 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
 545 550 555 560

20 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr  
 565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
 580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605

25 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640

30 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685

35 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
 705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735

5 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
 740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
 755 760 765

Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 10 770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815

15 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
 820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
 835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
 20 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
 885 890

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 893 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 30 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45

5 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80

10 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
 115 120 125

15 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160

20 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
 180 185 190

Ile Pro Asp Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
 195 200 205

25 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240

30 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 275 280 285

35 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300

	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	Glu	Val	Pro	Ser	Phe
	305					310			315					320		
	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asn	Cys	Glu	Ile
					325				330					335		
5	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	Ala	Tyr	Tyr	Ile	Pro
					340			345						350		
	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Thr	Leu	Val	Leu	Ser
					355			360						365		
10	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln
					370			375						380		
	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Ile	Ser	Pro
					385			390			395				400	
	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
					405				410					415		
15	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly
					420				425					430		
	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu
					435			440						445		
20	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Asn	Tyr
					450			455						460		
	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser
					465			470			475				480	
	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu
					485				490					495		
25	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
					500				505					510		
	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
					515				520					525		
30	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe
					530			535						540		
	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu
					545			550						555		560
	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Glu	Tyr	Ser	Thr
					565				570					575		
35	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro
					580				585					590		

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 5 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 10 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700  
 15 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
 705 710 715 720  
 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735  
 20 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
 740 745 750  
 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
 755 760 765  
 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780  
 25 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800  
 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815  
 30 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
 820 825 830  
 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
 835 840 845  
 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
 850 855 860  
 35 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
 885 890

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 893 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: protein

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30

15 Asn Ala Val Tyr Asp Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu  
 35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys  
 50 55 60

20 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg  
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg  
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu  
 100 105 110

25 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu  
 115 120 125

Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
 130 135 140

30 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro  
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn  
 180 185 190

35 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu  
 195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu  
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile  
 225 230 235 240

5 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val  
 245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu  
 260 265 270

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln  
 10 275 280 285

Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His  
 290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe  
 305 310 315 320

15 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile  
 325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro  
 340 345 350

Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser  
 20 355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln  
 370 375 380

Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro  
 385 390 395 400

25 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro  
 405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly  
 420 425 430

Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu  
 30 435 440 445

Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr  
 450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480

35 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu  
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr  
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys  
 515 520 525

5 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe  
 530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu  
 545 550 555 560

10 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr  
 565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro  
 580 585 590

Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605

15 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620

Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640

20 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655

Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala  
 660 665 670

Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685

25 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu  
 705 710 715 720

30 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735

Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala  
 740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser  
 755 760 765

35 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815

5 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp  
                   820                  825                  830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val  
835 840 845

10 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu  
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val  
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser  
885 890

15 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu  
1 5 10 15

25 Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys  
                  20                         25                         30

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro  
35 40 45

30 Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr  
           50                   55                   60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu  
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser  
85 90 95

35 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val

	100	105	110
	Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala		
	115	120	125
	Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser		
5	130	135	140
	Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser		
	145	150	155
	Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp		
	165	170	175
10	Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu		
	180	185	190
	Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val		
	195	200	205
15	Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu		
	210	215	220
	Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu		
	225	230	235
	Glu Tyr Gly Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile		
	245	250	255
20	Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile		
	260	265	270
	Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr		
	275	280	285
25	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Ile Ala Asn Glu		
	290	295	300
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu		
	305	310	315
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr		
	325	330	335
30	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg		
	340	345	350
	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu		
	355	360	365
	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp		
35	370	375	380
	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala		
	385	390	395
			400

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile  
 405 410 415  
 Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu  
 420 425 430  
 5 Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser  
 435 440 445  
 Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile  
 450 455 460  
 10 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr  
 465 470 475 480  
 Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu  
 485 490 495  
 Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln  
 500 505 510  
 15 Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala  
 515 520 525  
 Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala  
 530 535 540  
 20 Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg  
 545 550 555 560  
 Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu  
 565 570 575  
 Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val  
 580 585 590  
 25 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser  
 595 600 605  
 Trp Ser  
 610

## (2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 1..14  
(D) OTHER INFORMATION: /note= "'Xaa' is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
10 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
20 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
30 (B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:15:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:16:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## 20 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:17:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## 30 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:18:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:19:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:20:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Pro Val Ala Phe Asp Ser Glu Thr Ser Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:21:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ile Val Ser Asp Ile Glu Ala Asn Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:22:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

20 (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACGTTCAA GCGCTAGGGC AAAAGA

26

## (2) INFORMATION FOR SEQ ID NO:23:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTATATTATA GAGTAGTTAA CCATCTTCC A

31

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10 Phe Leu Phe Asp Gly Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

20 Leu Leu Val Asp Gly His  
1 5

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

30 Ser Leu Ile Thr Gly Asp Lys Asp Met Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10 Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAGGCCAGG GCTGTGCCGG CAAAGAGAAA TAGTC

35

## 20 (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGCATATC CTTGGCGCCG GTTATTATGA AAATC

35

## (2) INFORMATION FOR SEQ ID NO:30:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCAAGACGG GTACCGCCAC TGGCAGGTTG

30

(2) INFORMATION FOR SEQ ID NO:31:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:32:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25 TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:33:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTTCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:34:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TATAGAGTAG TTAACCATCT TTCCAACCCG ATGCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:35:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGATGGTTA ACGCGTCTAT AATATAACGG

29

(2) INFORMATION FOR SEQ ID NO:36:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAGAGGCAC AGAGAGTTTC ACC

23

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATTATA GAGGAGTTAA CCATCTTCC

30

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 AAGATGGTTA ACTTCTCTAT AATATACGG

29

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

48

## (2) INFORMATION FOR SEQ ID NO:40:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATAGAGTAG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC

48

## 10 (2) INFORMATION FOR SEQ ID NO:41:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTGGCCGCC CGATGCATCA GGGGGTC

27

## (2) INFORMATION FOR SEQ ID NO:42:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGCCGCC CGCTTCATGA GGGGGTCCAC

30

## (2) INFORMATION FOR SEQ ID NO:43:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGCCGCC CTGTACATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 GTATATTATA GAGGTGTTAA CCATCTTCC

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

25 GGGAGACCGG AATTCTCCTT CATTAATTCC TATA

34

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGAGACCCT GGAACATATAG GAATTAATGA AGGAGAATTG CGGTCTCCCC

49

(2) INFORMATION FOR SEQ ID NO:47:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTATTTGGT ATGCTTGTGC

20

(2) INFORMATION FOR SEQ ID NO:48:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTATTTGGA ATATATGTGC CT

22

(2) INFORMATION FOR SEQ ID NO:49:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACGAACATTC TACAAGTTAC

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTCAGAGAA ACTGACCTGT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

20 GATAAAATGCC AAACATGTTG T

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCTCTCAGG ATTTCCCTCCA

20

## (2) INFORMATION FOR SEQ ID NO:53:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTGAGAC CTCTGTGTCC

20

## 10 (2) INFORMATION FOR SEQ ID NO:54:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTCAGAAGA AACAGTGATG GT

22

## (2) INFORMATION FOR SEQ ID NO:55:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGGAGTCGC AAGCTGAAGT AGC

23

## (2) INFORMATION FOR SEQ ID NO:56:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCCTGAGTGA CAGAGTGAGA ACC

23

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

15 CCCACTAGGT TGTAAGCTCC ATGA

24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TACTATGTGC CAGGCTCTGT CCTA

24

25 (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTCATGAAG GTGACAGTTC

20

(2) INFORMATION FOR SEQ ID NO:60:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGTTGTTGA CCTATTGCAT

20

(2) INFORMATION FOR SEQ ID NO:61:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCTCTGTTT CCTCCCTGTT

20

(2) INFORMATION FOR SEQ ID NO:62:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTATTGGCC TTGAAGGTAG

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCCCGTGTG GGAACCATGA CTG

23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

20 TACATAGCGA GACTCCATCT CCC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTATGCGAG CGTATGGATA

20

## (2) INFORMATION FOR SEQ ID NO:66:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CACCACCATT GATCTGGAAG

20

## 10 (2) INFORMATION FOR SEQ ID NO:67:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCAACCACAC TGGGAA

16

## (2) INFORMATION FOR SEQ ID NO:68:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACAGTTGCC CACGGT

16

## (2) INFORMATION FOR SEQ ID NO:69:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATGAAATGC TGACTGGGTA

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

15 TCAATTATG TGCAGCCAAT

20

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATAGCGAGA CTCCATCTCC

20

25 (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGAGAGGGC AAAGATCGAT

20

(2) INFORMATION FOR SEQ ID NO:73:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AACACTAGTG ACATTATTTT CA

22

(2) INFORMATION FOR SEQ ID NO:74:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGCTAGGCCT GAAGGCTTCT

20

(2) INFORMATION FOR SEQ ID NO:75:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCCTAGTGGA TGATAAGAAT AATC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGACAGATGA TAAATACATA GGATGGATGG

30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

20 TTCTCTTACA ACACGTCCCC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATTTGGATGG CTTGACAGAG

20

## (2) INFORMATION FOR SEQ ID NO:79:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACATTCTAAG ACTTTCCCAA T

21

## 10 (2) INFORMATION FOR SEQ ID NO:80:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGAGCATGCA CCCTGAATTG

20

## (2) INFORMATION FOR SEQ ID NO:81:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

25 (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGAACCATG CGATACGACT

20

## (2) INFORMATION FOR SEQ ID NO:82:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CATTCCTAGA TGGGTAAAGC

20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

15 GCTTAGTCAT ACGAGCGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCACAGCCA TGTAAACC

18

25 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CCCCGGAGCA AGTTCA

16

(2) INFORMATION FOR SEQ ID NO:86:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGCCCAAAG CCAGAGTTA

18

(2) INFORMATION FOR SEQ ID NO:87:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATATGTGAGT CAATTCCCCA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTATTAGTC AATGTTCTCC AG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAGCTGCCCT AGTCAGCAC

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20 GCTTCCGAGT GCAGGGTCACA

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATTCTGGGCG CACAAGAGTG A

21

## (2) INFORMATION FOR SEQ ID NO:92:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACATCTCCCC TACCGCTATA

20

## 10 (2) INFORMATION FOR SEQ ID NO:93:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAAGTTCAAC ATCCGGCCGA CCCGTCGCAT TTC

33